

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB#

132539

Requester's Full Name: Jeffrey E. Russel Examiner #: 62785 Date: 9-14-2004
Unit: 1654 Phone Number: 571-272-0969 Serial Number: 101607595
Mail Box and Bldg/Room Location: Results Format Preferred (circle): PAPER DISK E-MAIL

REN 3C18(mailbox), 3D19(office)

If more than one search is submitted, please prioritize searches in order of need.

MEJ

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Molecules That Home To Various Selected Organs Or Tissues

Inventors (please provide full names): E. Ruoslahti, R. Pasqualini

Earliest Priority Filing Date: 6-27-2003

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 336 (PTCAY6WCA) in STN, in the U.S. patent application sequence databases (pending, published, issued), and in Geneseq/Swissprot/PIR.

336-aa- 9 Thank you.

MEJ

JER

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2004, 08:31:59 ; Search time 39 Seconds
(without alignments)
72.812 Million cell updates/sec

Title: US-10-607-595-336
Perfect score: 62
Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaphage:*
17: sp_archaeophages:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	44	71.0	470	16	Q8PHB1	Q8phb1 xanthomonas
2	42	67.7	2105	12	Q68772	Q68772 simian hemo
3	41.5	66.9	728	10	Q943S8	Q943s8 oryza sativ
4	41.5	66.9	739	10	Q93W67	Q93w67 oryza sativ
5	41	66.1	96	16	Q935D2	Q935d2 salmonella
6	41	66.1	634	10	Q9S9P3	Q9s9p3 arabidopsis
7	41	66.1	634	10	Q9SAI1	Q9sail arabidopsis
8	41	66.1	662	10	O23064	O23064 arabidopsis
9	40.5	65.3	149	11	Q8BNE8	Q8bne8 mus musculu
10	40.5	65.3	685	5	O44402	O44402 caenorhabdi
11	40	64.5	131	16	Q7UY28	Q7uy28 rhodopirell
12	40	64.5	169	16	Q981N3	Q981n3 rhizobium l
13	40	64.5	194	4	Q9BX47	Q9bx47 homo sapien
14	40	64.5	202	4	Q9BX48	Q9bx48 homo sapien
15	40	64.5	275	4	Q8TC41	Q8tc41 homo sapien
16	40	64.5	315	11	Q8VGS9	Q8vgs9 mus musculu
17	40	64.5	315	17	Q8TIC5	Q8tic5 methanosarc
18	40	64.5	430	10	Q9FM87	Q9fm87 arabidopsis
19	40	64.5	802	5	O76727	O76727 strongyloce
20	40	64.5	827	11	Q91WH4	Q91wh4 mus musculu
21	40	64.5	827	11	Q8CEJ4	Q8cej4 mus musculu
22	40	64.5	1134	10	Q7XN92	Q7xn92 oryza sativ
23	40	64.5	1673	10	Q7XRI2	Q7xri2 oryza sativ
24	39.5	63.7	613	16	Q8YN26	Q8yn26 anabaena sp
25	39	62.9	75	17	Q8ZYN7	Q8zyn7 pyrobaculum
26	39	62.9	81	5	Q9U645	Q9u645 conus texti
27	39	62.9	81	5	Q9U646	Q9u646 conus texti
28	39	62.9	82	5	Q9U661	Q9u661 conus penna
29	39	62.9	161	11	Q9D4N6	Q9d4n6 mus musculu
30	39	62.9	163	11	Q8CC80	Q8cc80 mus musculu
31	39	62.9	201	6	Q7YS22	Q7ys22 sus scrofa
32	39	62.9	318	11	Q8BHC0	Q8bhc0 mus musculu
33	39	62.9	318	11	Q99NE4	Q99ne4 mus musculu
34	39	62.9	322	4	Q8TC18	Q8tc18 homo sapien
35	39	62.9	322	4	Q9UNF4	Q9unf4 homo sapien
36	39	62.9	322	4	Q9Y5Y7	Q9y5y7 homo sapien
37	39	62.9	434	17	Q8PVI3	Q8pvi3 methanosarc
38	39	62.9	453	5	Q19481	Q19481 caenorhabdi
39	39	62.9	504	2	P72236	P72236 pseudomonas
40	38.5	62.1	669	5	O18045	O18045 caenorhabdi
41	38	61.3	56	9	Q8SCE1	Q8scel vibrio harv
42	38	61.3	77	5	Q9BPA3	Q9bpa3 conus ventr
43	38	61.3	127	5	Q9V759	Q9v759 drosophila
44	38	61.3	153	4	O75704	O75704 homo sapien
45	38	61.3	236	16	Q7V708	Q7v708 prochloroco
46	38	61.3	237	16	Q7VA95	Q7va95 prochloroco
47	38	61.3	304	16	Q9HUQ1	Q9huq1 pseudomonas
48	38	61.3	329	4	Q96PL2	Q96pl2 homo sapien
49	38	61.3	329	11	O08524	O08524 mus musculu
50	38	61.3	333	10	Q8VWZ5	Q8vwz5 oryza sativ
51	38	61.3	333	10	Q42992	Q42992 oryza sativ
52	38	61.3	342	10	Q7XYT0	Q7xyt0 artemisia t
53	38	61.3	357	10	Q8RVQ7	Q8rvq7 musa acumin
54	38	61.3	394	10	Q7XYS8	Q7xys8 artemisia t
55	38	61.3	591	4	Q12867	Q12867 homo sapien
56	38	61.3	657	5	Q8MNS5	Q8mns5 caenorhabdi
57	38	61.3	683	5	Q8MNS4	Q8mns4 caenorhabdi

58	38	61.3	698	10	Q8W5J1	Q8w5j1 oryza sativ
59	38	61.3	698	10	Q7XD69	Q7xd69 oryza sativ
60	38	61.3	885	11	Q8CFS4	Q8cfs4 mus musculu
61	38	61.3	904	13	Q91977	Q91977 xenopus lae
62	38	61.3	906	4	Q9UPF9	Q9upf9 homo sapien
63	38	61.3	922	11	Q62646	Q62646 rattus norv
64	38	61.3	938	11	Q62683	Q62683 rattus norv
65	38	61.3	943	4	Q9UPF8	Q9upf8 homo sapien
66	38	61.3	943	11	Q62648	Q62648 rattus norv
67	38	61.3	966	13	O93338	O93338 apteronotus
68	38	61.3	1753	5	Q9BHW9	Q9bhw9 leishmania
69	38	61.3	2165	5	Q19791	Q19791 caenorhabdi
70	37.5	60.5	658	10	O65214	O65214 volvox cart
71	37	59.7	130	10	Q7XZC1	Q7xzc1 pisum sativ
72	37	59.7	130	10	Q7XZC0	Q7xzc0 pisum sativ
73	37	59.7	130	10	Q7XTK6	Q7xtk6 pisum sativ
74	37	59.7	142	10	Q7XZC4	Q7xzc4 medicago tr
75	37	59.7	142	13	Q9YHR4	Q9yhr4 ginglymosto
76	37	59.7	143	5	Q9W079	Q9w079 drosophila
77	37	59.7	151	5	Q9VZ21	Q9vz21 drosophila
78	37	59.7	166	16	Q8YGE4	Q8yge4 brucella me
79	37	59.7	170	16	Q8G1H9	Q8glh9 brucella su
80	37	59.7	183	9	Q8LTG6	Q8ltg6 streptococc
81	37	59.7	206	16	Q8Y2B8	Q8y2b8 ralstonia s
82	37	59.7	210	16	Q8YPV8	Q8ypv8 anabaena sp
83	37	59.7	210	16	Q8YJX1	Q8yjsx1 anabaena sp
84	37	59.7	231	16	Q8A5D5	Q8a5d5 bacteroides
85	37	59.7	245	8	Q8WF52	Q8wf52 venerupis p
86	37	59.7	245	8	Q7YF44	Q7yf44 venerupis (
87	37	59.7	245	8	Q7YF41	Q7yf41 venerupis (
88	37	59.7	245	8	Q7Y720	Q7y720 venerupis (
89	37	59.7	247	5	Q965G8	Q965g8 caenorhabdi
90	37	59.7	295	10	Q949H3	Q949h3 hevea brasi
91	37	59.7	295	10	Q8GUD7	Q8gud7 hevea brasi
92	37	59.7	303	16	Q7UWX1	Q7uwx1 rhodopirell
93	37	59.7	309	10	Q8GTD7	Q8gtd7 cicer ariet
94	37	59.7	334	10	Q84WR5	Q84wr5 arabidopsis
95	37	59.7	348	12	Q91TR9	Q91tr9 tupaia herp
96	37	59.7	494	16	Q9I1B3	Q9ilb3 pseudomonas
97	37	59.7	495	2	O52406	O52406 edwardsiell
98	37	59.7	510	4	Q9H846	Q9h846 homo sapien
99	37	59.7	510	4	Q96GM8	Q96gm8 homo sapien
100	37	59.7	510	4	Q8IWN5	Q8iwn5 homo sapien
101	37	59.7	511	11	Q8R5A4	Q8r5a4 mus musculu
102	37	59.7	511	11	Q9D2E2	Q9d2e2 mus musculu
103	37	59.7	529	5	Q9V386	Q9v386 drosophila
104	37	59.7	636	5	Q8IST1	Q8ist1 anopheles g
105	37	59.7	705	5	O45884	O45884 caenorhabdi
106	37	59.7	779	16	Q8A9S2	Q8a9s2 bacteroides
107	37	59.7	883	3	Q9P563	Q9p563 neurospora
108	37	59.7	1087	5	Q7YYP3	Q7yyp3 cryptospori
109	37	59.7	1440	10	Q9LV30	Q9lv30 arabidopsis
110	37	59.7	1442	3	Q8NKE0	Q8nke0 aspergillus
111	37	59.7	1492	10	Q9FHA3	Q9fha3 arabidopsis
112	36.5	58.9	326	10	Q8VYR1	Q8vyr1 arabidopsis
113	36	58.1	50	16	Q9PA67	Q9pa67 xylella fas
114	36	58.1	130	10	Q7X9N3	Q7x9n3 pisum sativ

115	36	58.1	140	10	O65387	O65387 arabidopsis
116	36	58.1	235	5	P91236	P91236 caenorhabdi
117	36	58.1	236	16	Q825E4	Q825e4 streptomyce
118	36	58.1	275	16	Q8PML0	Q8pml0 xanthomonas
119	36	58.1	275	16	Q8PAV8	Q8pav8 xanthomonas
120	36	58.1	276	17	Q97WM2	Q97wm2 sulfolobus
121	36	58.1	284	12	Q8V614	Q8v614 simian pico
122	36	58.1	290	16	Q9PLG9	Q9plg9 chlamydia m
123	36	58.1	292	10	Q8H8R6	Q8h8r6 oryza sativ
124	36	58.1	296	5	O44636	O44636 caenorhabdi
125	36	58.1	304	16	Q8P4H0	Q8p4h0 xanthomonas
126	36	58.1	308	10	Q40668	Q40668 oryza sativ
127	36	58.1	319	10	Q40667	Q40667 oryza sativ
128	36	58.1	320	10	Q42994	Q42994 oryza sativ
129	36	58.1	322	10	Q42995	Q42995 oryza sativ
130	36	58.1	323	10	Q42993	Q42993 oryza sativ
131	36	58.1	360	10	Q9FX51	Q9fx51 arabidopsis
132	36	58.1	381	16	Q8X9W2	Q8x9w2 escherichia
133	36	58.1	381	16	Q8CVB7	Q8cvb7 escherichia
134	36	58.1	381	16	Q88MT2	Q88mt2 pseudomonas
135	36	58.1	396	16	Q7UGP9	Q7ugp9 rhodopirell
136	36	58.1	414	16	Q82MC3	Q82mc3 streptomyce
137	36	58.1	432	16	Q82P08	Q82p08 streptomyce
138	36	58.1	460	8	Q94T84	Q94t84 diaphus spl
139	36	58.1	460	8	Q94TB0	Q94tb0 neoscopelus
140	36	58.1	528	5	Q9N967	Q9n967 leishmania
141	36	58.1	605	16	Q7VDF4	Q7vdf4 prochloroco
142	36	58.1	745	11	Q8K103	Q8k103 mus musculu
143	36	58.1	763	3	O60013	O60013 pneumocysti
144	36	58.1	773	10	Q9FZ72	Q9fz72 arabidopsis
145	36	58.1	848	5	Q9GUC7	Q9guc7 caenorhabdi
146	36	58.1	866	4	Q8IXF3	Q8ixf3 homo sapien
147	36	58.1	883	5	Q966A6	Q966a6 caenorhabdi
148	36	58.1	904	5	Q966A5	Q966a5 caenorhabdi
149	36	58.1	918	5	Q9GUC8	Q9guc8 caenorhabdi
150	36	58.1	969	11	Q7TS67	Q7ts67 mus musculu

ALIGNMENTS

RESULT 1

Q8PHB1

ID Q8PHB1 PRELIMINARY; PRT; 470 AA.
AC Q8PHB1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC3349.
GN XAC3349.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL; AE011981; AAM38191.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 470 AA; 48970 MW; 4050CCDB1917DBDB CRC64;

Query Match 71.0%; Score 44; DB 16; Length 470;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PTCAYGWC 8
 | || |||
 Db 112 PVCATGWC 119

Search completed: September 16, 2004, 08:36:50
 Job time : 46 secs

OM protein - protein search, using sw model

Run on: September 16, 2004, 08:31:24 ; Search time 9 Seconds
 (without alignments)
 52.070 Million cell updates/sec

Title: US-10-607-595-336
 Perfect score: 62
 Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	46	74.2	542	1	YIM1_YEAST	P40474	saccharomyc
2	42	67.7	417	1	SAHH_METTH	O27673	methanobact
3	40	64.5	826	1	VIL1_MOUSE	Q62468	mus musculu
4	39	62.9	30	1	CXOB_CONPE	P56713	conus penna
5	39	62.9	81	1	CXO4_CONTE	Q9xzl1	conus texti
6	39	62.9	342	1	FPP2_ARATH	Q43315	arabidopsis
7	39	62.9	384	1	FPP1_ARATH	Q09152	arabidopsis
8	38	61.3	329	1	TECB_CHICK	P54097	gallus gall
9	38	61.3	417	1	Z232_HUMAN	Q9uny5	homo sapien
10	38	61.3	601	1	YKH1_CAEEL	P34269	caenorhabdi
11	38	61.3	938	1	NMZ1_HUMAN	Q05586	homo sapien
12	38	61.3	938	1	NMZ1_MOUSE	P35438	mus musculu
13	38	61.3	938	1	NMZ1_RAT	P35439	rattus norv
14	37	59.7	130	1	ALB1_PEA	P08687	pisum sativ
15	37	59.7	392	1	OR1A_DROME	Q9w5g6	drosophila
16	37	59.7	473	1	FP2_MYTGA	Q25464	mytilus gal
17	37	59.7	503	1	KIR3_HUMAN	P37023	homo sapien

18	37	59.7	949	1	PMA6_ARATH	Q9sh76 arabidopsis
19	36	58.1	76	1	BB11_SCHCO	P78742 schizophyll
20	36	58.1	318	1	CHI1_ORYSA	P24626 oryza sativ
21	36	58.1	381	1	YDCS_ECOLI	P76108 escherichia
22	36	58.1	862	1	PGCV_MACNE	Q28858 macaca neme
23	36	58.1	870	1	SRC2_HUMAN	Q96gp6 homo sapien
24	36	58.1	979	1	CLS1_MOUSE	Q9ep12 mus musculu
25	36	58.1	2738	1	PGCV_RAT	Q9erb4 rattus norv
26	36	58.1	3358	1	PGCV_MOUSE	Q62059 mus musculu
27	36	58.1	3381	1	PGCV_BOVIN	P81282 bos taurus
28	36	58.1	3396	1	PGCV_HUMAN	P13611 homo sapien
29	36	58.1	3562	1	PGCV_CHICK	Q90953 gallus gall
30	35	56.5	110	1	PHNA_STRMU	Q02419 streptococc
31	35	56.5	111	1	PHNA_ECOLI	P16680 escherichia
32	35	56.5	154	1	KR94_HUMAN	Q9byq2 homo sapien
33	35	56.5	159	1	KR93_HUMAN	Q9byq3 homo sapien
34	35	56.5	159	1	KR98_HUMAN	Q9byq0 homo sapien
35	35	56.5	638	1	COOS_METKA	Q8txx3 methanopyru
36	35	56.5	981	1	CLS1_HUMAN	O94985 homo sapien
37	34.5	55.6	652	1	SYG_SCHPO	Q10179 schizosacch
38	34	54.8	54	1	SKK1_MESMA	Q967f9 mesobuthus
39	34	54.8	210	1	RGSH_CHICK	Q9pwa0 gallus gall
40	34	54.8	210	1	RGSH_HUMAN	Q9ugc6 homo sapien
41	34	54.8	210	1	RGSH_MOUSE	Q9qzb0 mus musculu
42	34	54.8	245	1	ATS4_BOVIN	Q9tt93 bos taurus
43	34	54.8	294	1	DEH1_MORSP	Q01398 moraxella s
44	34	54.8	303	1	CHIB_POPTR	P29031 populus tri
45	34	54.8	312	1	O2LB_HUMAN	Q8ng80 homo sapien
46	34	54.8	340	1	CHI6_POPTR	P16579 populus tri
47	34	54.8	350	1	FPPS_MAIZE	P49353 zea mays (m
48	34	54.8	411	1	YG4I_YEAST	P42942 saccharomyc
49	34	54.8	468	1	NAH_SCHPO	P36606 schizosacch
50	34	54.8	498	1	VNUC_IAZOH	P26076 influenza a
51	34	54.8	511	1	GUNB_PSEFL	P18126 pseudomonas
52	34	54.8	642	1	NA95_MOUSE	Q9r017 mus musculu
53	34	54.8	646	1	NA95_HUMAN	Q9ulx6 homo sapien
54	34	54.8	820	1	AD29_HUMAN	Q9ukf5 homo sapien
55	34	54.8	837	1	ATS4_HUMAN	O75173 homo sapien
56	34	54.8	1021	1	S123_HUMAN	P55017 homo sapien
57	34	54.8	1202	1	JAG2_RAT	P97607 rattus norv
58	34	54.8	1238	1	JAG2_HUMAN	Q9y219 homo sapien
59	34	54.8	1247	1	JAG2_MOUSE	Q9qye5 mus musculu
60	34	54.8	1254	1	ERB2_MESAU	Q60553 mesocricetu
61	34	54.8	4655	1	LRP2_HUMAN	P98164 homo sapien
62	33.5	54.0	205	1	NEF_HV1ZH	P05859 human immun
63	33.5	54.0	205	1	NEF_SIVCZ	P17664 chimpanzee
64	33.5	54.0	211	1	NEF_HV1OY	P20886 human immun
65	33.5	54.0	239	1	NEF_HV1SC	P05857 human immun
66	33	53.2	27	1	CX3E_CONPU	P56529 conus purpu
67	33	53.2	45	1	HEVP_HEVBR	P80359 hevea brasi
68	33	53.2	76	1	CX02_CONTE	Q9xzk9 conus texti
69	33	53.2	76	1	CX03_CONTE	Q9xzl0 conus texti
70	33	53.2	81	1	ALB1_LUPAN	Q96474 lupinus ang
71	33	53.2	89	1	ALB1_PHA AU	Q9frt8 phaseolus a
72	33	53.2	90	1	ALB1_PHA AN	Q9frt9 phaseolus a
73	33	53.2	119	1	ALB1_GLYSO	Q9zqx0 glycine soj
74	33	53.2	119	1	ALB1_SOYBN	Q39837 glycine max

75	33	53.2	121	1	CHIC_POPTR	P29032	populus tri
76	33	53.2	128	1	RNP_PREEN	P19644	presbytis e
77	33	53.2	179	1	XYNT_PSEXY	P83513	pseudobutyr
78	33	53.2	209	1	GTP1_MOUSE	P46425	mus musculu
79	33	53.2	209	1	GTP2_MOUSE	P19157	mus musculu
80	33	53.2	228	1	XYNA_BACPU	P00694	bacillus pu
81	33	53.2	254	1	V30K_HCMVE	P06724	human cytom
82	33	53.2	261	1	XYNA_CLOSA	P17137	clostridium
83	33	53.2	300	1	EXRN_BPT7	P00638	bacteriopha
84	33	53.2	302	1	EXRN_BPT3	P20321	bacteriopha
85	33	53.2	342	1	UL23_HCMVA	P16846	human cytom
86	33	53.2	343	1	YN93_ANASP	P46079	anabaena sp
87	33	53.2	345	1	YJ44_ARCFU	O28335	archaeoglob
88	33	53.2	353	1	WN11_XENLA	P49893	xenopus lae
89	33	53.2	354	1	WN11_BRARE	O73864	brachydanio
90	33	53.2	354	1	WN11_CHICK	P49339	gallus gall
91	33	53.2	354	1	WN11_COTJA	P51891	coturnix co
92	33	53.2	354	1	WN11_HUMAN	O96014	homo sapien
93	33	53.2	354	1	WN11_MOUSE	P48615	mus musculu
94	33	53.2	385	1	YEIB_ECOLI	P25747	escherichia
95	33	53.2	404	1	SAHH_THEMA	O51933	thermotoga
96	33	53.2	405	1	SAHH_ARCFU	O28279	archaeoglob
97	33	53.2	411	1	SAHH_METAC	Q8tra5	methanosarc
98	33	53.2	411	1	SAHH_METMA	Q8puq4	methanosarc
99	33	53.2	415	1	SAHH_METJA	Q58783	methanococc
100	33	53.2	418	1	SAHH_AQUAE	O67240	aquifex aeo
101	33	53.2	421	1	SAHH_PYRFU	P50251	pyrococcus
102	33	53.2	421	1	SAHH_PYRHO	O58275	pyrococcus
103	33	53.2	422	1	SAHH_PYRAB	Q9uyk5	pyrococcus
104	33	53.2	424	1	SAHH_METKA	P58855	methanopyru
105	33	53.2	425	1	SAHH_ANASP	Q8yx05	anabaena sp
106	33	53.2	425	1	SAHH_SYNY3	P74008	synechocyst
107	33	53.2	426	1	SYH_PROMM	Q7v4p3	prochloroco
108	33	53.2	429	1	SAHH_SYNEL	Q8dgc8	synechococc
109	33	53.2	442	1	SECY_SYNY3	P77964	synechocyst
110	33	53.2	448	1	YG4Q_YEAST	P50079	saccharomyc
111	33	53.2	512	1	XYNA_CLOSR	P33558	clostridium
112	33	53.2	563	1	YIMO_YEAST	P40475	saccharomyc
113	33	53.2	577	1	TERL_BPSF5	P59217	bacteriopha
114	33	53.2	581	1	YHJ2_YEAST	P38767	saccharomyc
115	33	53.2	607	1	XYNA_NEOPA	P29127	neocallimas
116	33	53.2	630	1	ATS4_RAT	Q9esp7	rattus norv
117	33	53.2	652	1	SSP1_SCHPO	P50526	schizosacch
118	33	53.2	672	1	HYFB_ECOLI	P23482	escherichia
119	33	53.2	716	1	BGAL_THETU	P26257	thermoanaer
120	33	53.2	717	1	TRD1_ECOLI	P09130	escherichia
121	33	53.2	722	1	AD21_HUMAN	Q9ukj8	homo sapien
122	33	53.2	738	1	TRD2_ECOLI	P22708	escherichia
123	33	53.2	826	1	VIL1_HUMAN	P09327	homo sapien
124	33	53.2	828	1	LGR6_HUMAN	Q9hbx8	homo sapien
125	33	53.2	892	1	HIC1_MOUSE	Q9rly5	mus musculu
126	33	53.2	954	1	XYNA_RUMFL	P29126	ruminococcu
127	33	53.2	982	1	MSH2_SCHPO	O74773	schizosacch
128	33	53.2	1002	1	S123_MOUSE	P59158	mus musculu
129	33	53.2	1002	1	S123_RAT	P55018	rattus norv
130	33	53.2	1216	1	DPG1_RAT	Q9qyv8	rattus norv
131	33	53.2	1239	1	DPG1_HUMAN	P54098	homo sapien

132	33	53.2	1239	1	DPG1_MOUSE	P54099	mus musculus
133	33	53.2	1243	1	DPOA_ORYSA	O48653	oryza sativ
134	33	53.2	1670	1	CA34_HUMAN	Q01955	homo sapien
135	33	53.2	2335	1	TOR1_SCHPO	O14356	schizosacch
136	33	53.2	2337	1	TOR2_SCHPO	Q9y7k2	schizosacch
137	33	53.2	2476	1	ZAN_PIG	Q28983	sus scrofa
138	32.5	52.4	215	1	Y093_TREPA	O83131	treponema p
139	32.5	52.4	345	1	TAR4_HUMAN	Q96ri8	homo sapien
140	32.5	52.4	355	1	YM79_YEAST	Q04018	saccharomyc
141	32.5	52.4	376	1	PSPB_RAT	P22355	rattus norv
142	32.5	52.4	471	1	P2X2_HUMAN	Q9ubl9	homo sapien
143	32.5	52.4	733	1	ACE1_TRIRE	Q9p8w3	trichoderma
144	32	51.6	17	1	CXMA_CONPE	P58926	conus penna
145	32	51.6	17	1	CXMB_CONPE	P58927	conus penna
146	32	51.6	54	1	SKK2_MESMA	Q95nk7	mesobuthus
147	32	51.6	54	1	SKK3_MESMA	Q9bjx2	mesobuthus
148	32	51.6	73	1	BB13_SCHCO	P78744	schizophyll
149	32	51.6	100	1	TXOB_ATRIL	Q9bjv7	atrax sp. i
150	32	51.6	102	1	TXOA_HADIN	Q9bjv9	hadronyche

ALIGNMENTS

RESULT 1

YIM1_YEAST

ID YIM1_YEAST STANDARD; PRT; 542 AA.

AC P40474;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical 59.6 kDa protein in KGD1-SIM1 intergenic region.

GN YIL121W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RX MEDLINE=97313266; PubMed=9169870;

RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,

RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,

RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,

RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,

RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";

RL Nature 387:84-87(1997).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN

CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE

CC CARI/CYHR SUBFAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----

DR EMBL; Z46833; CAA86871.1; -.
DR PIR; S49888; S49888.
DR GermOnline; 139656; -.
DR SGD; S0001383; YIL121W.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PROSITE; PS50850; MFS; 1.
KW Hypothetical protein; Transport; Transmembrane.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 217 237 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 334 354 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
FT TRANSMEM 438 458 POTENTIAL.
FT TRANSMEM 473 493 POTENTIAL.
FT TRANSMEM 504 524 POTENTIAL.
SQ SEQUENCE 542 AA; 59617 MW; 96649B74E940F63E CRC64;

Query Match 74.2%; Score 46; DB 1; Length 542;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAYGWC 8
|||||
Db 426 CAYGWC 431

Search completed: September 16, 2004, 08:36:02
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 08:34:59 ; Search time 15 Seconds
(without alignments)
57.715 Million cell updates/sec

Title: US-10-607-595-336
Perfect score: 62
Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
1	46	74.2	542	2	S49888	probable membrane
2	42	67.7	417	2	F69085	adenosylhomocystei
3	41	66.1	634	2	E96840	hypothetical prote
4	41	66.1	634	2	E86293	T24D18.1 protein -
5	41	66.1	662	2	T01533	hypothetical prote
6	40.5	65.3	685	2	T32571	hypothetical prote
7	39.5	63.7	613	2	AH2398	hypothetical prote
8	39	62.9	342	2	S71182	farnesyl-pyrophosp
9	39	62.9	343	2	S52009	farnesyl-pyrophosp
10	39	62.9	453	2	T20965	hypothetical prote
11	39	62.9	635	2	A54592	110k actin filamen
12	38.5	62.1	669	2	T24571	hypothetical prote
13	38	61.3	304	2	B83032	probable permease

14	38	61.3	329	2	A57246	beta-tectorin prec
15	38	61.3	484	2	S44739	C02C2.1 protein -
16	38	61.3	681	2	T16353	hypothetical prote
17	38	61.3	885	2	JN0339	N-methyl-D-asparta
18	38	61.3	901	2	JN0337	N-methyl-D-asparta
19	38	61.3	906	2	A46296	N-methyl-D-asparta
20	38	61.3	906	2	JN0341	N-methyl-D-asparta
21	38	61.3	922	2	JN0340	N-methyl-D-asparta
22	38	61.3	922	2	JN0338	N-methyl-D-asparta
23	38	61.3	938	2	S19710	N-methyl-D-asparta
24	38	61.3	938	2	A46612	N-methyl-D-asparta
25	38	61.3	938	2	S21104	N-methyl-D-asparta
26	38	61.3	943	2	A47551	N-methyl-D-asparta
27	38	61.3	959	2	JN0336	N-methyl-D-asparta
28	38	61.3	2165	2	T21371	hypothetical prote
29	37.5	60.5	658	2	T08153	cysteine proteinas
30	37	59.7	130	2	A25014	albumin precursor
31	37	59.7	166	2	AI3403	hypothetical membr
32	37	59.7	210	2	AC2316	transposase alr408
33	37	59.7	210	2	AD2570	transposase all855
34	37	59.7	247	2	T33654	hypothetical prote
35	37	59.7	473	2	A56175	adhesive plaque pr
36	37	59.7	494	2	B83351	conserved hypothet
37	37	59.7	503	2	A49431	activin/TGF-beta-1
38	37	59.7	705	2	T34477	hypothetical prote
39	37	59.7	883	2	T49781	related to mutanas
40	37	59.7	949	2	G84486	probable plasma me
41	36	58.1	50	2	E82529	hypothetical prote
42	36	58.1	140	2	A86254	hypothetical prote
43	36	58.1	147	2	T25680	hypothetical prote
44	36	58.1	154	2	T49466	hypothetical prote
45	36	58.1	235	2	T25681	hypothetical prote
46	36	58.1	276	2	E90388	hypothetical prote
47	36	58.1	290	1	D81738	probable 3',5'-cyc
48	36	58.1	308	2	JC2253	chitinase (EC 3.2.
49	36	58.1	314	2	T32672	hypothetical prote
50	36	58.1	318	2	S14948	chitinase (EC 3.2.
51	36	58.1	319	2	JC2252	chitinase (EC 3.2.
52	36	58.1	322	2	S54806	chitinase (EC 3.2.
53	36	58.1	323	2	T03614	chitinase (EC 3.2.
54	36	58.1	381	2	D90884	probable transport
55	36	58.1	381	2	C85734	probable transport
56	36	58.1	381	2	C64896	Putative ABC trans
57	36	58.1	773	2	D86268	F13B4.3 protein -
58	36	58.1	848	2	B89042	protein F14F9.3 [i
59	36	58.1	862	2	S43922	versican - pig-tai
60	36	58.1	918	2	A89042	protein F14F9.4 [i
61	36	58.1	1643	2	T14274	versican precursor
62	36	58.1	2397	1	A55535	versican precursor
63	36	58.1	2409	1	A60979	versican precursor
64	36	58.1	3381	2	T42389	versican precursor
65	36	58.1	3562	2	A47171	chondroitin sulfat
66	35	56.5	33	2	D44798	alkylphosphonate u
67	35	56.5	111	2	B35718	alkylphosphonate u
68	35	56.5	111	2	B91265	alkylphosphonate u
69	35	56.5	111	2	G86105	alkylphosphonate u
70	35	56.5	114	2	A95385	protein [imported

71	35	56.5	183	2	T10508	hypothetical prote
72	35	56.5	185	2	AB2241	hypothetical prote
73	35	56.5	251	2	AH3314	hypothetical membr
74	35	56.5	302	2	C84470	hypothetical prote
75	35	56.5	345	2	T34476	hypothetical prote
76	35	56.5	346	2	AF3334	metal chelate tran
77	35	56.5	434	2	T26275	hypothetical prote
78	35	56.5	507	2	A83105	probable fumarase
79	35	56.5	507	2	C81063	fumarate hydratase
80	35	56.5	546	2	A81807	fumarate hydratase
81	35	56.5	551	2	G82630	fumarate hydratase
82	35	56.5	816	2	A71006	hypothetical prote
83	35	56.5	1171	2	T31635	hypothetical prote
84	34.5	55.6	596	2	T23084	hypothetical prote
85	34.5	55.6	607	2	T23085	hypothetical prote
86	34.5	55.6	652	2	T38704	glycyl tRNA synthe
87	34.5	55.6	677	2	T23083	hypothetical prote
88	34	54.8	81	2	T29888	hypothetical prote
89	34	54.8	82	2	T29889	hypothetical prote
90	34	54.8	82	2	T29893	hypothetical prote
91	34	54.8	82	2	T29891	hypothetical prote
92	34	54.8	84	2	T33867	hypothetical prote
93	34	54.8	102	2	T10199	hypothetical prote
94	34	54.8	125	2	T02519	hypothetical prote
95	34	54.8	177	2	C95865	conserved hypothet
96	34	54.8	276	2	T29894	hypothetical prote
97	34	54.8	294	2	A44856	haloacetate dehalo
98	34	54.8	327	2	A81839	probable periplasm
99	34	54.8	327	2	D81103	hypothetical prote
100	34	54.8	336	1	S18750	chitinase (EC 3.2.
101	34	54.8	340	2	S48030	probable chitinase
102	34	54.8	350	2	T03291	farnesyl-pyrophosp
103	34	54.8	353	2	T03687	farnesyl-pyrophosp
104	34	54.8	356	2	D95925	probable membrane-
105	34	54.8	379	2	PC4180	thiazide-sensitive
106	34	54.8	384	2	T20446	hypothetical prote
107	34	54.8	411	2	S53933	probable membrane
108	34	54.8	464	2	C86422	probable glycyl-tR
109	34	54.8	468	2	S20951	Na ⁺ /H ⁺ -exchanging
110	34	54.8	484	2	T26190	hypothetical prote
111	34	54.8	498	2	A83635	conserved hypothet
112	34	54.8	503	2	AC0062	conserved hypothet
113	34	54.8	511	2	S10527	endoglucanase B pr
114	34	54.8	584	2	I50419	s-glycerin precurs
115	34	54.8	837	2	T00355	hypothetical prote
116	34	54.8	1021	2	G01202	NaCl electroneutra
117	34	54.8	1254	2	I48161	p-185 precursor -
118	33.5	54.0	205	1	B44963	nef protein - huma
119	33.5	54.0	205	1	ASLJIK	nef protein - simi
120	33.5	54.0	226	2	S46353	nef protein - simi
121	33.5	54.0	317	2	T25003	hypothetical prote
122	33.5	54.0	629	2	T22066	hypothetical prote
123	33.5	54.0	919	2	T21049	hypothetical prote
124	33	53.2	24	2	A58999	psi-conotoxin PIII
125	33	53.2	45	2	S50180	pseudo-hevein - Pa
126	33	53.2	50	2	H82423	hypothetical prote
127	33	53.2	54	2	F72675	hypothetical prote

128	33	53.2	74	2	T31295	hypothetical prote
129	33	53.2	78	2	T50943	probable ferredoxi
130	33	53.2	81	2	H85691	unknown protein en
131	33	53.2	96	2	A81031	hypothetical prote
132	33	53.2	98	2	A28918	hypothetical prote
133	33	53.2	116	2	T10993	NADH2 dehydrogenas
134	33	53.2	119	2	S48192	insulin-like growt
135	33	53.2	121	2	S18751	chitinase (EC 3.2.
136	33	53.2	126	2	A82519	hypothetical prote
137	33	53.2	128	2	A33083	pancreatic ribonuc
138	33	53.2	134	2	E82953	conserved hypothet
139	33	53.2	148	2	H83054	suppressor protein
140	33	53.2	209	1	A55140	glutathione transf
141	33	53.2	210	1	B55140	glutathione transf
142	33	53.2	212	2	C96718	hypothetical prote
143	33	53.2	220	2	B49736	collagen alpha 3(I
144	33	53.2	228	1	WWBSXP	endo-1,4-beta-xyla
145	33	53.2	228	2	S03050	Ig gamma chain (cl
146	33	53.2	245	2	B86738	hypothetical prote
147	33	53.2	249	2	T31061	hypothetical prote
148	33	53.2	254	1	WMBECT	major early 30K pr
149	33	53.2	261	1	S12745	endo-1,4-beta-xyla
150	33	53.2	264	1	B69413	conserved hypothet

ALIGNMENTS

RESULT 1

S49888

probable membrane protein YIL121w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein YI8277.08

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 19-Apr-2002

C;Accession: S49888

R;Hamlyn, N.; Churcher, C.

submitted to the EMBL Data Library, November 1994

A;Reference number: S49881

A;Accession: S49888

A;Molecule type: DNA

A;Residues: 1-542 <HAM>

A;Cross-references: GB:Z47047; EMBL:Z46833; NID:g603997; PID:g763225;

GSPDB:GN00009; MIPS:YIL121w

C;Genetics:

A;Gene: MIPS:YIL121w

A;Cross-references: SGD:S0001383

A;Map position: 9L

C;Superfamily: yeast probable membrane protein YIL121w

C;Keywords: transmembrane protein

F;72-88/Domain: transmembrane #status predicted <TM1>

F;98-114/Domain: transmembrane #status predicted <TM2>

F;129-145/Domain: transmembrane #status predicted <TM3>

F;154-170/Domain: transmembrane #status predicted <TM4>

F;191-207/Domain: transmembrane #status predicted <TM5>

F;221-237/Domain: transmembrane #status predicted <TM6>

F;301-317/Domain: transmembrane #status predicted <TM7>

F;339-355/Domain: transmembrane #status predicted <TM8>

F;440-456/Domain: transmembrane #status predicted <TM9>
F;477-493/Domain: transmembrane #status predicted <TM10>
F;508-524/Domain: transmembrane #status predicted <TM11>

Query Match 74.2%; Score 46; DB 2; Length 542;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAYGWC 8
|||||
Db 426 CAYGWC 431

Search completed: September 16, 2004, 08:37:30
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 08:36:55 ; Search time 128 Seconds
(without alignments)
22.580 Million cell updates/sec

Title: US-10-607-595-336
Perfect score: 62
Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	47	75.8	206	12	US-10-424-599-256189	Sequence 256189,
2	42	67.7	56	12	US-10-424-599-281235	Sequence 281235,
3	42	67.7	78	9	US-09-749-637A-324	Sequence 324, App
4	42	67.7	417	15	US-10-369-493-21527	Sequence 21527, A
5	41.5	66.9	63	9	US-09-864-761-39829	Sequence 39829, A
6	41.5	66.9	653	16	US-10-437-963-192047	Sequence 192047,
7	41	66.1	30	9	US-09-749-637A-92	Sequence 92, Appl
8	41	66.1	77	9	US-09-749-637A-119	Sequence 119, App
9	40	64.5	30	9	US-09-749-637A-89	Sequence 89, Appl
10	40	64.5	93	9	US-09-925-297-749	Sequence 749, App
11	39	62.9	32	9	US-09-749-637A-140	Sequence 140, App
12	39	62.9	34	9	US-09-749-637A-137	Sequence 137, App
13	39	62.9	82	9	US-09-749-637A-125	Sequence 125, App
14	39	62.9	82	9	US-09-749-637A-128	Sequence 128, App
15	39	62.9	82	9	US-09-749-637A-131	Sequence 131, App
16	39	62.9	82	9	US-09-749-637A-134	Sequence 134, App
17	39	62.9	82	9	US-09-749-637A-282	Sequence 282, App
18	39	62.9	93	15	US-10-242-355-387	Sequence 387, App
19	39	62.9	173	12	US-10-424-599-191056	Sequence 191056,
20	39	62.9	175	11	US-09-764-875-773	Sequence 773, App
21	39	62.9	255	10	US-09-866-050A-700	Sequence 700, App
22	39	62.9	297	15	US-10-138-588-2	Sequence 2, Appli
23	39	62.9	322	9	US-09-909-320-201	Sequence 201, App
24	39	62.9	322	9	US-09-909-088B-201	Sequence 201, App
25	39	62.9	322	9	US-09-905-291A-201	Sequence 201, App
26	39	62.9	322	9	US-09-902-853-201	Sequence 201, App
27	39	62.9	322	9	US-09-907-824-201	Sequence 201, App
28	39	62.9	322	9	US-09-907-841-201	Sequence 201, App
29	39	62.9	322	10	US-09-904-011-201	Sequence 201, App
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32	39	62.9	322	10	US-09-907-613-201	Sequence 201, App
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34	39	62.9	322	10	US-09-904-859-201	Sequence 201, App
35	39	62.9	322	10	US-09-909-204-201	Sequence 201, App
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106	39	62.9	322	12	US-10-298-993-201	Sequence 201, App
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108	39	62.9	322	12	US-10-448-923-201	Sequence 201, App
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110	39	62.9	322	13	US-10-063-547-6	Sequence 6, Appli
111	39	62.9	322	14	US-10-063-616-6	Sequence 6, Appli
112	39	62.9	322	14	US-10-063-502-6	Sequence 6, Appli
113	39	62.9	322	14	US-10-063-518-6	Sequence 6, Appli

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115	39	62.9	322	14	US-10-227-693-6	Sequence 6, Appli
116	39	62.9	322	14	US-10-063-567-6	Sequence 6, Appli
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118	39	62.9	322	14	US-10-063-599-6	Sequence 6, Appli
119	39	62.9	322	14	US-10-063-595-6	Sequence 6, Appli
120	39	62.9	322	14	US-10-223-085-32	Sequence 32, Appl
121	39	62.9	322	14	US-10-223-084-32	Sequence 32, Appl
122	39	62.9	322	14	US-10-223-088-32	Sequence 32, Appl
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131	39	62.9	322	14	US-10-223-089-32	Sequence 32, Appl
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135	39	62.9	322	14	US-10-063-586-6	Sequence 6, Appli
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147	39	62.9	322	14	US-10-063-686-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1

US-10-424-599-256189

; Sequence 256189, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 256189
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7335C.1.pep
US-10-424-599-256189

Query Match 75.8%; Score 47; DB 12; Length 206;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAYGWCA 9
|| ||||:
Db 199 TCIYGWCS 206

Search completed: September 16, 2004, 08:47:53
Job time : 131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 08:32:44 ; Search time 17 Seconds
(without alignments)
27.331 Million cell updates/sec

Title: US-10-607-595-336
Perfect score: 62
Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	62	100.0	9	3	US-09-258-754-336	Sequence 336, App
2	62	100.0	9	3	US-09-042-107-336	Sequence 336, App
3	62	100.0	9	4	US-09-722-250D-336	Sequence 336, App
4	41	66.1	194	4	US-09-252-991A-24154	Sequence 24154, A
5	40.5	65.3	169	4	US-09-252-991A-22543	Sequence 22543, A
6	40	64.5	202	4	US-09-252-991A-27017	Sequence 27017, A
7	39	62.9	318	4	US-09-724-864-60	Sequence 60, Appl
8	39	62.9	322	2	US-08-892-880-2	Sequence 2, Appli
9	39	62.9	322	4	US-09-232-160-21	Sequence 21, Appl
10	39	62.9	322	4	US-09-907-794A-201	Sequence 201, App
11	39	62.9	322	4	US-09-905-125A-201	Sequence 201, App

12	39	62.9	322	4	US-09-902-775A-201	Sequence 201, Appl
13	38	61.3	100	1	US-08-189-199A-3	Sequence 3, Appli
14	38	61.3	101	1	US-08-189-199A-4	Sequence 4, Appli
15	38	61.3	169	4	US-09-252-991A-24746	Sequence 24746, A
16	38	61.3	262	4	US-09-252-991A-22359	Sequence 22359, A
17	38	61.3	266	4	US-08-311-731A-112	Sequence 112, App
18	38	61.3	305	4	US-09-252-991A-33032	Sequence 33032, A
19	38	61.3	777	2	US-08-231-193A-16	Sequence 16, Appl
20	38	61.3	777	2	US-08-486-273A-16	Sequence 16, Appl
21	38	61.3	777	3	US-08-480-474-16	Sequence 16, Appl
22	38	61.3	777	3	US-08-940-086A-16	Sequence 16, Appl
23	38	61.3	777	4	US-08-940-035A-16	Sequence 16, Appl
24	38	61.3	777	4	US-08-935-105A-16	Sequence 16, Appl
25	38	61.3	777	4	US-09-648-797-16	Sequence 16, Appl
26	38	61.3	777	4	US-09-386-123-16	Sequence 16, Appl
27	38	61.3	854	2	US-08-231-193A-32	Sequence 32, Appl
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31	38	61.3	854	4	US-08-940-035A-32	Sequence 32, Appl
32	38	61.3	854	4	US-08-935-105A-32	Sequence 32, Appl
33	38	61.3	854	4	US-09-648-797-32	Sequence 32, Appl
34	38	61.3	854	4	US-09-386-123-32	Sequence 32, Appl
35	38	61.3	863	3	US-08-436-332B-2	Sequence 2, Appli
36	38	61.3	870	2	US-08-231-193A-30	Sequence 30, Appl
37	38	61.3	870	2	US-08-486-273A-30	Sequence 30, Appl
38	38	61.3	870	3	US-08-480-474-30	Sequence 30, Appl
39	38	61.3	870	3	US-08-940-086A-30	Sequence 30, Appl
40	38	61.3	870	4	US-08-940-035A-30	Sequence 30, Appl
41	38	61.3	870	4	US-08-935-105A-30	Sequence 30, Appl
42	38	61.3	870	4	US-09-648-797-30	Sequence 30, Appl
43	38	61.3	870	4	US-09-386-123-30	Sequence 30, Appl
44	38	61.3	875	2	US-08-231-193A-28	Sequence 28, Appl
45	38	61.3	875	2	US-08-486-273A-28	Sequence 28, Appl
46	38	61.3	875	3	US-08-480-474-28	Sequence 28, Appl
47	38	61.3	875	3	US-08-940-086A-28	Sequence 28, Appl
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50	38	61.3	875	4	US-09-648-797-28	Sequence 28, Appl
51	38	61.3	875	4	US-09-386-123-28	Sequence 28, Appl
52	38	61.3	885	4	US-08-264-578-11	Sequence 11, Appl
53	38	61.3	885	4	US-08-217-704C-10	Sequence 10, Appl
54	38	61.3	885	4	US-08-164-487A-2	Sequence 2, Appli
55	38	61.3	891	2	US-08-231-193A-26	Sequence 26, Appl
56	38	61.3	891	2	US-08-486-273A-26	Sequence 26, Appl
57	38	61.3	891	3	US-08-480-474-26	Sequence 26, Appl
58	38	61.3	891	3	US-08-940-086A-26	Sequence 26, Appl
59	38	61.3	891	4	US-08-940-035A-26	Sequence 26, Appl
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64	38	61.3	906	4	US-08-164-487A-29	Sequence 29, Appl
65	38	61.3	908	2	US-08-231-193A-34	Sequence 34, Appl
66	38	61.3	908	2	US-08-486-273A-34	Sequence 34, Appl
67	38	61.3	908	3	US-08-480-474-34	Sequence 34, Appl
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69	38	61.3	908	4	US-08-940-035A-34	Sequence 34, Appl
70	38	61.3	908	4	US-08-935-105A-34	Sequence 34, Appl
71	38	61.3	908	4	US-09-648-797-34	Sequence 34, Appl
72	38	61.3	908	4	US-09-386-123-34	Sequence 34, Appl
73	38	61.3	920	1	US-08-026-138E-9	Sequence 9, Appli
74	38	61.3	920	1	US-08-026-138E-10	Sequence 10, Appl
75	38	61.3	922	2	US-08-231-193A-14	Sequence 14, Appl
76	38	61.3	922	2	US-08-231-193A-20	Sequence 20, Appl
77	38	61.3	922	2	US-08-486-273A-14	Sequence 14, Appl
78	38	61.3	922	2	US-08-486-273A-20	Sequence 20, Appl
79	38	61.3	922	3	US-08-480-474-14	Sequence 14, Appl
80	38	61.3	922	3	US-08-480-474-20	Sequence 20, Appl
81	38	61.3	922	3	US-08-940-086A-14	Sequence 14, Appl
82	38	61.3	922	3	US-08-940-086A-20	Sequence 20, Appl
83	38	61.3	922	4	US-08-940-035A-14	Sequence 14, Appl
84	38	61.3	922	4	US-08-940-035A-20	Sequence 20, Appl
85	38	61.3	922	4	US-08-935-105A-14	Sequence 14, Appl
86	38	61.3	922	4	US-08-935-105A-20	Sequence 20, Appl
87	38	61.3	922	4	US-09-648-797-14	Sequence 14, Appl
88	38	61.3	922	4	US-09-648-797-20	Sequence 20, Appl
89	38	61.3	922	4	US-08-217-704C-24	Sequence 24, Appl
90	38	61.3	922	4	US-08-164-487A-28	Sequence 28, Appl
91	38	61.3	922	4	US-09-386-123-14	Sequence 14, Appl
92	38	61.3	922	4	US-09-386-123-20	Sequence 20, Appl
93	38	61.3	927	4	US-08-217-704C-21	Sequence 21, Appl
94	38	61.3	927	4	US-08-164-487A-25	Sequence 25, Appl
95	38	61.3	929	2	US-08-231-193A-40	Sequence 40, Appl
96	38	61.3	929	2	US-08-486-273A-40	Sequence 40, Appl
97	38	61.3	929	3	US-08-480-474-40	Sequence 40, Appl
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103	38	61.3	938	2	US-08-231-193A-2	Sequence 2, Appli
104	38	61.3	938	2	US-08-486-273A-2	Sequence 2, Appli
105	38	61.3	938	3	US-08-480-474-2	Sequence 2, Appli
106	38	61.3	938	3	US-08-940-086A-2	Sequence 2, Appli
107	38	61.3	938	4	US-08-940-035A-2	Sequence 2, Appli
108	38	61.3	938	4	US-08-935-105A-2	Sequence 2, Appli
109	38	61.3	938	4	US-09-648-797-2	Sequence 2, Appli
110	38	61.3	938	4	US-09-386-123-2	Sequence 2, Appli
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124	38	61.3	959	3	US-08-940-086A-24	Sequence 24, Appl
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142	38	61.3	985	4	US-08-217-704C-28	Sequence 28, Appl
143	38	61.3	985	4	US-08-164-487A-31	Sequence 31, Appl
144	38	61.3	985	4	US-08-164-487A-32	Sequence 32, Appl
145	38	61.3	997	2	US-08-231-193A-38	Sequence 38, Appl
146	38	61.3	997	2	US-08-486-273A-38	Sequence 38, Appl
147	38	61.3	997	3	US-08-480-474-38	Sequence 38, Appl
148	38	61.3	997	3	US-08-940-086A-38	Sequence 38, Appl
149	38	61.3	997	4	US-08-940-035A-38	Sequence 38, Appl
150	38	61.3	997	4	US-08-935-105A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-258-754-336

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; Sequence 336, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 336
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-336
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Query Match          100.0%; Score 62; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGWCA 9
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Db 1 PTCAYGWCA 9

RESULT 2

US-09-042-107-336

; Sequence 336, Application US/09042107

; Patent No. 6232287

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

; TITLE OF INVENTION: Tissues

; FILE REFERENCE: P-LJ 2892

; CURRENT APPLICATION NUMBER: US/09/042,107

; CURRENT FILING DATE: 1998-03-13

; NUMBER OF SEQ ID NOS: 436

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 336

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-042-107-336

Query Match 100.0%; Score 62; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGWCA 9
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Db 1 PTCAYGWCA 9

RESULT 3

US-09-722-250D-336

; Sequence 336, Application US/09722250D

; Patent No. 6610651

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

; TITLE OF INVENTION: Tissues

; FILE REFERENCE: P-LJ 4514

; CURRENT APPLICATION NUMBER: US/09/722,250D

; CURRENT FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: US 09/042,107

; PRIOR FILING DATE: 1998-03-13

; NUMBER OF SEQ ID NOS: 437

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 336

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-336

Query Match 100.0%; Score 62; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGWCA 9
| | | | | | | | |
Db 1 PTCAYGWCA 9

RESULT 4

US-09-252-991A-24154
; Sequence 24154, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24154
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24154

Query Match 66.1%; Score 41; DB 4; Length 194;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAYGWCA 9
| | | | |
Db 187 CASGWCA 193

Search completed: September 16, 2004, 08:37:06
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 08:29:34 ; Search time 53 Seconds
(without alignments)
47.980 Million cell updates/sec

Title: US-10-607-595-336
Perfect score: 62
Sequence: 1 PTCAYGWCA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqpl980s:*
2: geneseqpl990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query						
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2	62	100.0	9	5	AAU98819		Aau98819 Lymph nod	
3	42	67.7	35	4	ABG21634		Abg21634 Novel hum	
4	42	67.7	78	4	AAU06005		Aau06005 Cone snai	
5	41.5	66.9	63	4	AAM19964		Aam19964 Peptide #	
6	41.5	66.9	63	4	ABB40010		Abb40010 Peptide #	
7	41.5	66.9	63	4	AAM33631		Aam33631 Peptide #	
8	41.5	66.9	63	4	ABB24531		Abb24531 Protein #	
9	41.5	66.9	63	4	AAM73429		Aam73429 Human bon	

10	41.5	66.9	63	4	AAM60757	Aam60757	Human bra
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13	41	66.1	30	4	AAU05849	Aau05849	Cone snai
14	41	66.1	56	4	AAU63322	Aau63322	Propionib
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16	41	66.1	62	4	AAM82962	Aam82962	Human imm
17	41	66.1	65	4	AAU64444	Aau64444	Propionib
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20	41	66.1	65	6	ABM60963	Abm60963	Propionib
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23	40	64.5	60	4	ABB16612	Abb16612	Human ner
24	40	64.5	93	3	AAB54297	Aab54297	Human pan
25	40	64.5	198	4	ABG11786	Abg11786	Novel hum
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27	39	62.9	12	6	AAE34576	Aae34576	Phage pep
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43	39	62.9	297	6	ABU69126	Abu69126	Human NOV
44	39	62.9	305	3	AAG29734	Aag29734	Arabidops
45	39	62.9	318	4	AAE05364	Aae05364	Mouse lym
46	39	62.9	322	2	AAW56249	Aaw56249	Amino aci
47	39	62.9	322	2	AAy13379	Aay13379	Amino aci
48	39	62.9	322	3	AAy87287	Aay87287	Human sig
49	39	62.9	322	3	ADC78521	Adc78521	Human PRO
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51	39	62.9	322	4	AAB87528	Aab87528	Human PRO
52	39	62.9	322	4	AAB88391	Aab88391	Human mem
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55	39	62.9	322	5	ABB84832	Abb84832	Human PRO
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61	39	62.9	322	6	ABU90878	Abu90878	Novel hum
62	39	62.9	322	6	ABO33937	Abo33937	Human sec
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66	39	62.9	322	6	ABU71508	Abu71508	Human sec

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69	39	62.9	322	6	ABO27283	Abo27283	Human	sec
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93	39	62.9	322	6	ABO34169	Abo34169	Human	sec
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96	39	62.9	322	6	ADA00337	Ada00337	Human	sec
97	39	62.9	322	7	ADA16661	Ada16661	Human	sec
98	39	62.9	322	7	ADA13090	Ada13090	Human	sec
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136	39	62.9	322	8	ADE73379	Ade73379	Human	sec
137	39	62.9	322	8	ADE41282	Ade41282	Human	sec
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139	39	62.9	322	8	ADE73914	Ade73914	Human	sec
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145	38	61.3	18	5	AAU90561	Aau90561	Insulin/i	
146	38	61.3	18	5	AAU90884	Aau90884	Insulin/i	
147	38	61.3	47	4	AAM92224	Aam92224	Human	dig
148	38	61.3	54	4	AAU61417	Aau61417	Propionib	
149	38	61.3	54	6	ABM57936	Abm57936	Propionib	
150	38	61.3	70	4	AAU05989	Aau05989	Cone snai	

ALIGNMENTS

RESULT 1

AAY48970

ID AAY48970 standard; peptide; 9 AA.

XX

AC AAY48970;

XX

DT 20-MAR-2003 (revised)

DT 10-DEC-1999 (first entry)

XX

DE Membrane dipeptidase-binding lymph node homing peptide #44.

XX

KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;

KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

KW membrane dipeptidase.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9946284-A2.

XX

PD 16-SEP-1999.

XX

PF 10-MAR-1999; 99WO-US005284.

XX

PR 13-MAR-1998; 98US-00042107.

PR 26-FEB-1999; 99US-00258754.
XX
PA (BURN-) BURNHAM INST.
XX
PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX
DR WPI; 1999-571717/48.
XX
PT New peptides which selectively home to organs or tissues, used for, e.g.
PT identifying target ligands and for therapy of pathological conditions.
XX
PS Claim 78; Page 153; 193pp; English.
XX
CC The present invention describes peptides that selectively home to a
CC tissue or organ. The peptides can be used for identifying an organ or
CC tissue, for identifying a target molecule expressed by an organ or tissue
CC or for treating an organ or tissue pathology, where the organ or tissue
CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
CC used in the exemplification of the present invention. (Updated on 20-MAR-
CC 2003 to correct PR field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 62; DB 2; Length 9;
Best Local Similarity 100.0%; Pred.. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGWCA 9
| | | | | | | |
Db 1 PTCAYGWCA 9

RESULT 2

AAU98819

ID AAU98819 standard; peptide; 9 AA.

XX

AC AAU98819;

XX

DT 22-AUG-2002 (first entry)

XX

DE Lymph node targeting peptide #1.

XX

KW Targeting peptide; cancer; lymph node targeting; cytostatic; anti-HIV;
KW immunostimulant; immunogen; cancer; human immunodeficiency virus; HIV;
KW vector delivery.

XX

OS Synthetic.

XX

PN WO200220724-A2.

XX

PD 14-MAR-2002.

XX

PF 07-SEP-2001; 2001WO-US028045.

XX

PR 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-489672/52.
 XX
 PT Modulation of immune system response comprises administration of
 PT targeting peptide attached to immunogen.
 XX
 PS Claim 8; Fig 7; 86pp; English.
 XX
 CC This invention relates to a method for modulating the immune system
 CC response comprising administration of a lymph node targeting peptide
 CC attached to an immunogen. The invention also comprises a bispecific
 CC compound comprising the sequences Cys-Ala-Tyr or Ser-Cys-Ala-Arg, a
 CC bispecific compound comprising a targeting peptide attached to a vector
 CC binding moiety and a method for targeting a vector to an organ or tissue
 CC comprising administering the vector and a complex comprising a targeting
 CC peptide and a binding moiety. The peptides of the invention may have
 CC cytostatic, anti-HIV or immunostimulant activities. The method of the
 CC invention is useful for increasing the immune response to an immunogen,
 CC especially a cancer cell or human immunodeficiency virus (HIV). The
 CC method is useful for the selective delivery of gene therapy vectors. The
 CC present sequence represents lymph node homing peptide used in the method
 CC of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 62; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGWCA 9
 |||||
 Db 1 PTCAYGWCA 9

RESULT 3
 ABG21634
 ID ABG21634 standard; protein; 35 AA.
 XX
 AC ABG21634;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21625.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS85821.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 51993; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 35 AA;

Query Match 67.7%; Score 42; DB 4; Length 35;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTCAYGW 7
|:|:|
Db 11 PSCSYGW 17

Search completed: September 16, 2004, 08:35:54
Job time : 64 secs

\$%^STN;HighlightOn= ***;HighlightOff=*** ;
=> d his

(FILE 'HOME' ENTERED AT 07:41:20 ON 16 SEP 2004)

L1 FILE 'REGISTRY' ENTERED AT 07:41:29 ON 16 SEP 2004
1 S PTCAYGWCA/SQSP

L2 FILE 'CAPLUS' ENTERED AT 07:41:52 ON 16 SEP 2004
3 S L1

=> fil reg

FILE 'REGISTRY' ENTERED AT 07:42:53 ON 16 SEP 2004
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STRUCTURE FILE UPDATES: 14 SEP 2004 HIGHEST RN 744786-72-9
DICTIONARY FILE UPDATES: 14 SEP 2004 HIGHEST RN 744786-72-9

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> d que l1

L1 1 SEA FILE=REGISTRY ABB=ON PLU=ON PTCAYGWCA/SQSP

=> d sqide3 l1 1

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 243962-03-0 REGISTRY
CN L-Alanine, L-prolyl-L-threonyl-L-cysteinyl-L-alanyl-L-tyrosylglycyl-L-
tryptophyl-L-cysteinyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 9

SEQ3 1 Pro-Thr-Cys-Ala-Tyr-Gly-Trp-Cys-Ala
=== === === === === === === ===

HITS AT: 1-9

MF C43 H58 N10 O12 S2
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
DT.CA CAPLUS document type: Journal; Patent
RL.P Roles from patents: BIOL (Biological study); PREP (Preparation); PRP
(Properties); USES (Uses)
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

Absolute stereochemistry.

/ Structure 1 in file .gra /

/ Structure 2 in file .gra /

3 REFERENCES IN FILE CA (1907 TO DATE)
3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> fil caplus

FILE 'CAPLUS' ENTERED AT 07:43:12 ON 16 SEP 2004

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FILE COVERS 1907 - 16 Sep 2004 VOL 141 ISS 12

FILE LAST UPDATED: 15 Sep 2004 (20040915/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

=> d que nos 12

L1 1 SEA FILE=REGISTRY ABB=ON PLU=ON PTCAYGWCA/SQSP

L2 3 SEA FILE=CAPLUS ABB=ON PLU=ON L1

=> d .ca 12 1-3

L2 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:185278 CAPLUS

DOCUMENT NUMBER: 136:241645

TITLE: Adenoviral targeting and manipulation of immune system response using targeting peptides

INVENTOR(S): Arap, Wadih; Pasqualini, Renata

PATENT ASSIGNEE(S): Board of Regents, the University of Texas System, USA

SOURCE: PCT Int. Appl., 86 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002020724	A2	20020314	WO 2001-US28045	20010907
WO 2002020724	A3	20020711		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2001090663 A5 20020322 AU 2001-90663 20010907
 EP 1315512 A2 20030604 EP 2001-970682 20010907

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

WO 2004020999 A1 20040311 WO 2002-US34987 20021030

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

US 2000-231266P P 20000908
 US 2001-765101 A 20010117
 US 2001-97651 A 20010117
 WO 2001-US28045 W 20010907
 WO 2002-US27836 A 20020830

AB The present invention concerns compns. and methods relating to the identification and use of targeting peptides. Such targeting peptides selectively home to specific organs or tissues in vivo. The novel targeting sequences disclosed herein are of use for the targeted delivery of various therapeutic agents to the targeted organ or tissue. In particular embodiments, the present invention concerns bispecific targeting reagents comprising an organ targeting peptide attached to a mol., such as a Fab fragment, that binds to a gene therapy vector or other therapeutic agent. In alternative embodiments, bispecific targeting peptides contg. an organ targeting moiety and a gene therapy or therapeutic agent targeting moiety may be obtained and used for targeted delivery. Other embodiments concern modulation of host immune system function through the targeted delivery of antigens or other mols. to lymph nodes. Numerous examples of targeting peptide sequences against adenovirus or lymph node tissue are disclosed herein.

IC ICM C12N

CC 1-6 (Pharmacology)

Section cross-reference(s): 15, 63

IT 18635-55-7P 85530-39-8P 168179-57-5P 184240-25-3P 184240-26-4P
 184240-32-2P 243961-35-5P 243961-97-9P ***243962-03-0P***
 286380-02-7P 286380-06-1P 403981-35-1P 403981-36-2P 403981-37-3P
 403981-38-4P 403981-39-5P 403981-40-8P 403981-41-9P 403981-42-0P
 403981-43-1P 403981-44-2P 403981-45-3P 403981-46-4P 403981-47-5P
 403981-48-6P 403981-49-7P 403981-50-0P 403981-51-1P

RL: PAC (Pharmacological activity); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(adenoviral targeting and manipulation of immune system response using targeting peptides)

L2 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2001:880210 CAPLUS

DOCUMENT NUMBER: 136:133251

TITLE: Modulation of the immune response by systemic targeting of antigens to lymph nodes

AUTHOR(S): Trepel, Martin; Arap, Wadih; Pasqualini, Renata

CORPORATE SOURCE: The University of Texas M. D. Anderson Cancer Center, Houston, TX, 77030, USA

SOURCE: Cancer Research (2001), 61(22), 8110-8112

CODEN: CNREA8; ISSN: 0008-5472

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Factors that det. the immunogenicity of an antigen in vivo are still largely unknown. Direct administration of antigens into lymphatic organs appears to enhance immune response. The authors hypothesized that systemically targeting antigens to lymphatic tissue in vivo might modulate immunity. To test this hypothesis, the authors measured the humoral immune response elicited by bacteriophage vaccination. The authors show that the responses against a lymph node-targeted phage are significantly higher than those against control untargeted phage; the effect is specific because it is inhibited by coadministration of the cognate synthetic peptides displayed. Our data suggest that systemic targeting of antigens to lymph nodes through the circulation modulates humoral immune response. This strategy may have broad applications in the development of vaccines, prodn. of antibodies, and immunotherapy.

CC 15-2 (Immunochemistry)

IT 243961-97-9 ***243962-03-0***

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(targeting to lymph node enhances its immunogenicity)

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:595206 CAPLUS

DOCUMENT NUMBER: 131:223515

TITLE: Molecules that home to various selected organs or tissues for therapeutic and diagnostic use

INVENTOR(S): Rajotte, Daniel; Pasqualini, Renata; Ruoslahti, Erkki I.

PATENT ASSIGNEE(S): The Burnham Institute, USA

SOURCE: PCT Int. Appl., 193 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9946284	A2	19990916	WO 1999-US5284	19990310
WO 9946284	A3	20000406		

W: AU, CA, JP

RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE

US 6232287	B1	20010515	US 1998-42107	19980313
US 6174687	B1	20010116	US 1999-258754	19990226
CA 2323071	AA	19990916	CA 1999-2323071	19990310
AU 9930783	A1	19990927	AU 1999-30783	19990310
AU 762991	B2	20030710		
EP 1062232	A2	20001227	EP 1999-912400	19990310

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, FI

JP 2002506079	T2	20020226	JP 2000-535660	19990310
US 6784153	B1	20040831	US 2000-676475	20000929
US 6610651	B1	20030826	US 2000-722250	20001122

PRIORITY APPLN. INFO.:

US 1998-42107	A	19980313
US 1999-258754	A	19990226
WO 1999-US5284	W	19990310

OTHER SOURCE(S): MARPAT 131:223515

AB Mols. are provided that selectively home to various normal organs or tissues, including to lung, pancreas, skin, retina, prostate, ovary, lymph node, adrenal gland, liver, and gut. Also provided are mols. that selectively home to tumor-bearing organs or tissues, including to pancreas bearing a pancreatic tumor or to lung bearing a lung tumor. The invention also provides conjugates, comprising an organ- or tissue-homing mol. linked to a moiety. Such a moiety can be e.g. a therapeutic agent or a detectable agent. The invention also provides a method of identifying a membrane dipeptidase (MDP)-binding homing mol. that selectively homes to lung endothelium. The method includes contacting MDP with one or more mols. and detg. specific binding of a mol. to the MDP, where the presence of specific binding identifies the mol. as a MDP-binding homing mol. that selectively homes to lung endothelium. Such MDP-binding homing mols. can be linked to a moiety and, when administered to a subject as a conjugate, can selectively direct the moiety to lung endothelium in the subject.

IC C07K007-06; C07K007-08; A61K038-08; A61K038-10; A61K031-195

CC 1-12 (Pharmacology)

Section cross-reference(s): 9, 34

IT 243961-35-5 243961-36-6 243961-37-7 243961-38-8 243961-39-9
243961-40-2 243961-41-3 243961-42-4 243961-43-5 243961-44-6
243961-45-7 243961-46-8 243961-47-9 243961-48-0 243961-51-5
243961-52-6 243961-53-7 243961-54-8 243961-55-9 243961-56-0
243961-57-1 243961-58-2 243961-59-3 243961-60-6 243961-61-7
243961-63-9 243961-64-0 243961-65-1 243961-66-2 243961-67-3
243961-68-4 243961-69-5 243961-70-8 243961-71-9 243961-72-0
243961-73-1 243961-74-2 243961-75-3 243961-76-4 243961-77-5
243961-78-6 243961-79-7 243961-80-0 243961-81-1 243961-82-2
243961-83-3 243961-84-4 243961-85-5 243961-86-6 243961-87-7
243961-88-8 243961-89-9 243961-90-2 243961-91-3 243961-92-4
243961-93-5 243961-94-6 243961-95-7 243961-96-8 243961-97-9
243961-98-0 243961-99-1 243962-00-7 243962-01-8 243962-02-9
243962-03-0 243962-04-1 243962-05-2 243962-06-3
243962-07-4 243962-08-5 243962-09-6 243962-10-9 243962-11-0
243962-12-1 243962-13-2 243962-14-3 243962-17-6 243962-18-7
243962-19-8 243962-20-1 243962-21-2 243962-22-3 243962-34-7

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(mols. that home to various selected organs or tissues for therapeutic and diagnostic use)